# The 31st Global and Local Infectious Diseases Research Seminar

This Seminar will be held English.

RCGLID OITA UNIVERSITY

**September 19,2024 16:00-17:00** **Venue: OITA Univ. RCGLID Meeting Room & Zoom**

## Speaker1:Kirill Kryukov (16:00-16:30)

**Associate Professor, Research Organization of Information and Systems, National Institute of Genetics**

### Using GenomeSync-GSTK for the analysis of metagenomes from urban environments in Japan

The Japanese Urban Microbiome project studies microbiome of surface samples from urban environments. During the last three years we collected 488 samples from cities all over Japan, and performed shotgun metagenomic sequencing. In addition to commonly used methods, we are utilizing our own system called GenomeSync-GSTK for analyzing these samples. The system consists of GenomeSync database and Genome Search Toolkit (GSTK), which together enable accurate taxonomic classification of metagenomic sequences. When applied to urban metagenomes, this system allows us to not only characterize bacterial content, but also to detect eukaryotic DNA, including fungi, plants and animals. We observe abundant human DNA in urban samples. For plants, we observe multiple seasonal waves corresponding to pollen seasons of different species. For animals, we can detect traces of bird and arthropod DNA. The GenomeSync-GSTK pipeline is an effective tool for characterizing shotgun metagenomic data, that offers better accuracy than other tools at the expense of longer calculation time.

## Speaker2:Rumiko Suzuki (16:30-17:00)

**Associate Professor, Department of Informatics, National Institute of Genetics Project**

### Large-scale genome rearrangement in Helicobacter pylori isolated from indigenous Americans

About 50% of the world's population is infected with Helicobacter pylori, a bacterium that causes gastrointestinal diseases. It is known that H. pylori shows many structural variations in its genome, such as inversions and translocations. Among them, some strains isolated from indigenous Americans have genome structures that significantly differ from typical H. pylori and are more similar to Helicobacter acinonychis, a species found in large felines such as lions and cheetahs. However, it remains a mystery why these strains are found in indigenous Americans. Previously, only a few complete genome sequences of such structurally variant strains were available. However, the international Helicobacter pylori Genome Project (HpGp) has added genomes with similar structural variations. This study aims to explore the mystery of large-scale genome rearrangement among H. pylori strains of indigenous Americans in combination with animal-derived microbiome samples.

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